

1600

**CRF Errors Edited by the STIC Systems  
Branch**

Serial Number: 09/759,152A

CRF Edit Date: 10/21/03  
Edited by: M

RECEIVED  
OCT 21 2003  
TECH CENTER 1600/2900

**ENTERED**

Realigned nucleic acid/amino acid numbers/text in cases where the sequence  
text "wrapped" to the next line

Corrected the SEQ ID NO. Sequence numbers edited were:

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Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID  
NO's edited:

---

Deleted: \_\_\_\_\_ invalid beginning/end-of-file text ; \_\_\_\_\_ page numbers

Inserted mandatory headings/numeric identifiers, specifically:

---

Moved responses to same line as heading/numeric identifier, specifically:

---

Other:

Sequence 10 - inserted hard returns

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1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/759,152A

DATE: 10/21/2003

TIME: 17:58:53

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\10212003\I759152A.raw

4 <110> APPLICANT: Palmer, Michelle A.J.  
 5       Gee, Melissa  
 6       Tillotson, Bonnie  
 7       Chang, Xiao-Jia  
 9 <120> TITLE OF INVENTION: Systems for Sensitive Detection of G-Protein Coupled  
 10      Receptor and Orphan Receptor Function Using Reporter  
 11      Enzyme Mutant Complementation  
 13 <130> FILE REFERENCE: 4085-235-27 CIP  
 15 <140> CURRENT APPLICATION NUMBER: US 09/759,152A  
 16 <141> CURRENT FILING DATE: 2001-01-16  
 18 <150> PRIOR APPLICATION NUMBER: US 09/654,499  
 19 <151> PRIOR FILING DATE: 2000-09-01  
 21 <150> PRIOR APPLICATION NUMBER: US 60/180,669  
 22 <151> PRIOR FILING DATE: 2000-02-07  
 24 <160> NUMBER OF SEQ ID NOS: 10  
 26 <170> SOFTWARE: PatentIn version 3.0  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 6700  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Unknown  
 33 <220> FEATURE:  
 34 <223> OTHER INFORMATION: pICAST ALC.  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: CDS  
 38 <222> LOCATION: (1457)..(4486)  
 40 <400> SEQUENCE: 1  
 41 ctgcagcctg aatatggcc aaacaggata tctgtggtaa gcagttcctg ccccggtca                   60  
 43 gggccaagaa cagatggAAC agctgaatat gggccaaaca ggatatctgt ggtaaggagt                   120  
 45 tcctgccccg gctcaggccc aagaacagat ggtccccaga tgcggtccag ccctcagcag                   180  
 47 tttcttagaga accatcagat gtttccaggg tgccccaaagg acctgaaatg accctgtgcc                   240  
 49 ttatttgaac taaccaatca gttcgcttct cgcttctgtt cgcgcgcttc tgctccccga                   300  
 51 gctcaataaa agagcccaca acccctcaact cggggcgcca gtcctccgat tgactgagtc                   360  
 53 gccccggtaC ccgtgttatcc aataaaccct ctgcagttg catccgactt gtggtctcgc                   420  
 55 tgttccttgg gagggtctcc tctgagtgtat tgactacccg tcagcgggggg tctttcattt                   480  
 57 gggggctcgt ccgggatcgg gagacccctg cccagggacc accgaccac caccgggagg                   540  
 58 caagctggcc agcaacttat ctgtgtctgt ccgattgtct agtgtctatg actgattta                   600  
 62 tgcgcctgCG tcggtaact ttagctaact agctctgtat ctggcggacc cgtggtgaa                   660  
 64 ctgacgagtt ctgaacacccc ggccgcaacc ctgggagacg tcccaggac tttgggggCC                   720  
 66 gtttttgtgg cccgacctga ggaaggagC cgatgtggaa tccgaccccg tcaggatatg                   780  
 68 tggttctgggt aggagacgag aacctaaaac agttcccgcc tccgtctgaa tttttgcttt                   840  
 70 cggtttggaa ccgaagccgc gcgtcttgc tgcgtcagca tcgttctgt tttgtctgt                   900  
 72 ccgactgtgt ttctgtattt gtctgaaaat tagggccaga ctgttaccac tcccttaagt                   960  
 74 ttgaccttag gtaactggaa agatgtcgag cgctcgctc acaaccagtc ggtagatgtc                   1020

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76	aagaagagac	gttgggttac	cttctgctct	gcagaatggc	caacccttaa	cgtcgatgg	1080
78	ccgcgagacg	gcacccttaa	ccgagacacc	atcacccagg	ttaagatcaa	ggtctttca	1140
80	cctggcccgc	atggacacacc	agaccaggc	ccctacatcg	tgacctggga	agccttggct	1200
82	tttgcacccccc	ctccctgggt	caagccctt	gtacacccta	agcctccgcc	tcctcttcct	1260
84	ccatccgccc	cgtctctccc	cattgaacct	cctcggtcga	ccccgcctcg	atcctccctt	1320
86	tatccagccc	tcactccttc	tctaggcgcc	ggccgctcta	gcccattaat	acgactcact	1380
88	atagggcgat	tcgaatcagg	cattggcgcg	ccggatcctt	aattaagcgc	aattggagg	1440
90	tggcgtagc	ctcgag	atg	ggc	gtg	att	acg
				aat	gtc	ata	gtc
				gtc	gtc	gtc	gtc
				gtc	gtc	gtc	gtc
91				Met	Gly	Val	Ile
				1	5	10	
92							
94	cgc acc gat	cgc cct	tcc caa	cag tta	cgc agc	ctg aat	ggc gaa
95	Arg Thr Asp Arg	Pro Ser Gln	Gln Leu	Arg Ser	Leu Asn	Gly Glu	Trp
96	15		20		25		
98	cgc ttt	gcc tgg	ttt ccg	gca cca	gaa gcg	gtg ccg	gaa agc
99	Arg Phe Ala Trp	Phe Pro Ala	Pro Glu	Ala Val	Pro Glu	Ser Trp	Leu
100	30		35		40		
102	gag tgc	gat ctt	cct gag	gcc gat	act gtc	gtc ccc	tca aac
103	Glu Cys Asp	Leu Pro	Glu Ala Asp	Thr Val	Val Val	Pro Ser	Asn Trp
104	45		50		55		60
106	cag atg	cac ggt	tac gat	gct ccc	atc tac	acc aac	gtg acc tat
107	Gln Met His	Gly Tyr Asp	Ala Pro Ile	Tyr Thr Asn	Val Thr	Tyr Tyr	Pro
108	65		70		75		
110	att acg	gtc aat	ccg ccg	ttt gtt	ccc acg	gag aat	ccg acg
111	Ile Thr Val	Asn Pro	Pro Phe	Val Pro	Thr Glu	Asn Pro	Thr Gly
112	80		85		90		
114	tac tcg	ctc aca	ttt aat	gtt gat	gaa agc	tgg cta	cag gaa
115	Tyr Ser	Leu Thr	Phe Asn	Val Asp	Glu Ser	Trp Leu	Gln Glu
116	95		100		105		
117	acg cga	att att	ttt gat	ggc gtt	aac tcg	gcg ttt	cat ctg
118	Thr Arg Ile	Ile Phe	Asp Gly	Val Asn	Ser Ala	Phe His	Leu Trp
119	110		115		120		
123	aac ggg	cgc tgg	gtc ggt	tac ggc	cag gac	agt cgt	ttg ccg
124	Asn Gly Arg	Trp Val	Gly Tyr	Gly Gln	Asp Ser	Arg Leu	Pro Ser
125	125		130		135		140
127	ttt gac	ctg agc	gca ttt	tta cgc	gcc gga	gaa aac	cgc ctc
128	Phe Asp	Leu Ser	Ala Phe	Leu Arg	Ala Gly	Glu Asn	Arg Leu
129	145		150		155		
131	atg gtg	ctg cgc	tgg agt	gac ggc	agt tat	ctg gaa	gat cag
132	Met Val	Leu Arg	Trp Ser	Asp Gly	Ser Tyr	Leu Glu	Asp Gln
133	160		165		170		
135	tgg cgg	atg agc	ggc att	ttc cgt	gac gtc	tcg ttg	ctg cat
136	Trp Arg Met	Ser Gly	Ile Phe	Arg Asp	Val Ser	Leu Leu	His Lys
137	175		180		185		
139	act aca	caa atc	agc gat	ttc cat	gtt gcc	act cgc	ttt aat
140	Thr Thr Gln	Ile Ser Asp	Phe His	Val Ala	Thr Arg	Phe Asn	Asp Asp
141	190		195		200		
143	ttc agc	cgc gct	gta ctg	gag gct	gaa gtt	cag atg	tgc ggc
144	Phe Ser Arg	Ala Val	Leu Glu	Ala Glu	Val Gln	Met Cys	Gly Glu
145	205		210		215		220

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147	cgt gac tac cta cg	gta aca gtt tct tta tgg cag ggt gaa acg cag	2164
148	Arg Asp Tyr Leu Arg Val Thr Val Ser Leu Trp Gln Gly Glu Thr Gln		
149	225	230	235
151	gtc gcc agc ggc acc gc	cct ttc ggc ggt gaa att atc gat gag cgt	2212
152	Val Ala Ser Gly Thr Ala Pro Phe Gly Gly Glu Ile Ile Asp Glu Arg		
153	240	245	250
155	ggt ggt tat gcc gat cgc gtc aca cta cgt ctg aac gtc gaa aac ccg		2260
156	Gly Gly Tyr Ala Asp Arg Val Thr Leu Arg Leu Asn Val Glu Asn Pro		
157	255	260	265
159	aaa ctg tgg agc gcc gaa atc ccg aat ctc tat cgt gcg gtg gtt gaa		2308
160	Lys Leu Trp Ser Ala Glu Ile Pro Asn Leu Tyr Arg Ala Val Val Glu		
161	270	275	280
163	ctg cac acc gcc gac ggc acg ctg att gaa gca gaa gcc tgc gat gtc		2356
164	Leu His Thr Ala Asp Gly Thr Leu Ile Glu Ala Glu Ala Cys Asp Val		
165	285	290	295
167	ggt ttc cgc gag gtg cg	att gaa aat ggt ctg ctg ctg aac ggc	2404
168	Gly Phe Arg Glu Val Arg Ile Glu Asn Gly Leu Leu Leu Asn Gly		
169	305	310	315
171	aag ccg ttg ctg att cga ggc gtt aac cgt cac gag cat cat cct ctg		2452
172	Lys Pro Leu Leu Ile Arg Gly Val Asn Arg His Glu His His Pro Leu		
173	320	325	330
175	cat ggt cag gtc atg gat gag cag acg atg gtg cag gat atc ctg ctg		2500
176	His Gly Gln Val Met Asp Glu Gln Thr Met Val Gln Asp Ile Leu Leu		
177	335	340	345
179	atg aag cag aac aac ttt aac gcc gtg cgc tgt tcg cat tat ccg aac		2548
180	Met Lys Gln Asn Asn Phe Asn Ala Val Arg Cys Ser His Tyr Pro Asn		
181	350	355	360
184	cat ccg ctg tgg tac acg ctg tgc gac cgc tac ggc ctg tat gtg gtg		2596
185	His Pro Leu Trp Tyr Thr Leu Cys Asp Arg Tyr Gly Leu Tyr Val Val		
186	365	370	375
188	gat gaa gcc aat att gaa acc cac ggc atg gtg cca atg aat cgt ctg		2644
189	Asp Glu Ala Asn Ile Glu Thr His Gly Met Val Pro Met Asn Arg Leu		
190	385	390	395
192	acc gat gat ccg cgc tgg cta ccg gcg atg agc gaa cgc gta acg cga		2692
193	Thr Asp Asp Pro Arg Trp Leu Pro Ala Met Ser Glu Arg Val Thr Arg		
194	400	405	410
196	atg gtg cag cgc gat cgt aat cac ccg agt gtg atc atc tgg tcg ctg		2740
197	Met Val Gln Arg Asp Arg Asn His Pro Ser Val Ile Ile Trp Ser Leu		
198	415	420	425
200	ggg aat gaa tca ggc cac ggc gct aat cac gac gcg ctg tat cgc tgg		2788
201	Gly Asn Glu Ser Gly His Gly Ala Asn His Asp Ala Leu Tyr Arg Trp		
202	430	435	440
204	atc aaa tct gtc gat cct tcc cgc ccg gtg cag tat gaa ggc ggc gga		2836
205	Ile Lys Ser Val Asp Pro Ser Arg Pro Val Gln Tyr Glu Gly Gly		
206	445	450	455
208	gcc gac acc acg gcc acc gat att att tgc ccg atg tac gcg cgc gtg		2884
209	Ala Asp Thr Thr Ala Thr Asp Ile Ile Cys Pro Met Tyr Ala Arg Val		
210	465	470	475
212	gat gaa gac cag ccc ttc ccg gct gtg ccg aaa tgg tcc atc aaa aaa		2932

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213	Asp	Glu	Asp	Gln	Pro	Phe	Pro	Ala	Val	Pro	Lys	Trp	Ser	Ile	Lys	Lys
214		480				485						490				
216	tgg	ctt	tcg	cta	cct	gga	gag	acg	cgc	ccg	ctg	atc	ctt	tgc	gaa	tac
217	Trp	Leu	Ser	Leu	Pro	Gly	Glu	Thr	Arg	Pro	Leu	Ile	Leu	Cys	Glu	Tyr
218		495						500					505			
220	gcc	cac	gcf	atg	ggt	aac	agt	ctt	ggc	ggt	ttc	gct	aaa	tac	tgg	cag
221	Ala	His	Ala	Met	Gly	Asn	Ser	Leu	Gly	Gly	Phe	Ala	Lys	Tyr	Trp	Gln
222		510					515					520				
224	gcf	ttt	cgt	cag	tat	ccc	cgt	tta	cag	ggc	ggc	ttc	gtc	tgg	gac	tgg
225	Ala	Phe	Arg	Gln	Tyr	Pro	Arg	Leu	Gln	Gly	Gly	Phe	Val	Trp	Asp	Trp
226		525					530					535			540	
228	gtg	gat	cag	tcg	ctg	att	aaa	tat	gat	gaa	aac	ggc	aac	ccg	tgg	tcg
229	Val	Asp	Gln	Ser	Leu	Ile	Lys	Tyr	Asp	Glu	Asn	Gly	Asn	Pro	Trp	Ser
230						545				550			555			
232	gct	tac	ggc	ggt	gat	ttt	ggc	gat	acg	ccg	aac	gat	cgc	cag	ttc	tgt
233	Ala	Tyr	Gly	Gly	Asp	Phe	Gly	Asp	Thr	Pro	Asn	Asp	Arg	Gln	Phe	Cys
234						560			565			570				
236	atg	aac	ggt	ctg	gtc	ttt	gcc	gac	cgc	ccg	cat	cca	gcg	ctg	acg	
237	Met	Asn	Gly	Leu	Val	Phe	Ala	Asp	Arg	Thr	Pro	His	Pro	Ala	Leu	Thr
238		575				580			585							
240	gaa	gca	aaa	cac	cag	cag	ttt	ttc	cag	ttc	cgt	tta	tcc	ggg	caa	
241	Glu	Ala	Lys	His	Gln	Gln	Phe	Phe	Gln	Phe	Arg	Leu	Ser	Gly	Gln	
242		590				595			600							
245	acc	atc	gaa	gtg	acc	agc	gaa	tac	ctg	ttc	cgt	cat	agc	gat	aac	gag
246	Thr	Ile	Glu	Val	Thr	Ser	Glu	Tyr	Leu	Phe	Arg	His	Ser	Asp	Asn	Glu
247		605				610			615			620				
249	ctc	ctg	cac	tgg	atg	gtg	gcf	ctg	gat	ggt	aag	ccg	ctg	gca	agc	ggt
250	Leu	Leu	His	Trp	Met	Val	Ala	Leu	Asp	Gly	Lys	Pro	Leu	Ala	Ser	Gly
251						625			630			635				
253	gaa	gtg	cct	ctg	gat	gtc	gct	cca	caa	ggt	aaa	cag	ttg	att	gaa	ctg
254	Glu	Val	Pro	Leu	Asp	Val	Ala	Pro	Gln	Gly	Lys	Gln	Leu	Ile	Glu	Leu
255						640			645			650				
257	cct	gaa	cta	ccg	cag	ccg	gag	agc	gcc	ggg	caa	ctc	tgg	ctc	aca	gta
258	Pro	Glu	Leu	Pro	Gln	Pro	Glu	Ser	Ala	Gly	Gln	Leu	Trp	Leu	Thr	Val
259		655				660			665							
261	cgc	gta	gtg	caa	ccg	aac	gcf	acc	gca	tgg	tca	gaa	gcc	ggg	cac	atc
262	Arg	Val	Val	Gln	Pro	Asn	Ala	Thr	Ala	Trp	Ser	Glu	Ala	Gly	His	Ile
263		670				675			680							
265	agc	gcc	tgg	cag	cag	tgg	cgt	ctg	gcf	gaa	aac	ctc	agt	gtg	acg	ctc
266	Ser	Ala	Trp	Gln	Gln	Trp	Arg	Leu	Ala	Glu	Asn	Leu	Ser	Val	Thr	Leu
267		685				690			695			700				
269	ccc	gcc	gcf	tcc	cac	gcc	atc	ccg	cat	ctg	acc	acc	agc	gaa	atg	gat
270	Pro	Ala	Ala	Ser	His	Ala	Ile	Pro	His	Leu	Thr	Thr	Ser	Glu	Met	Asp
271						705			710			715				
273	ttt	tgc	atc	gag	ctg	ggt	aat	aag	cgt	tgg	caa	ttt	aac	ccg	cag	tca
274	Phe	Cys	Ile	Glu	Leu	Gly	Asn	Lys	Arg	Trp	Gln	Phe	Asn	Arg	Gln	Ser
275			720				725			730						
277	ggc	ttt	ctt	tca	cag	atg	tgg	att	ggc	gat	aaa	aaa	caa	ctg	ctg	acg
278	Gly	Phe	Leu	Ser	Gln	Met	Trp	Ile	Gly	Asp	Lys	Lys	Gln	Leu	Leu	Thr

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279	735	740	745		3748
281	ccg ctg cgc gat cag ttc acc cgt gca ccg ctg gat aac gac att ggc				
282	Pro Leu Arg Asp Gln Phe Thr Arg Ala Pro Leu Asp Asn Asp Ile Gly				
283	750	755	760		3796
285	gta agt gaa gcg acc cgc att gac cct aac gcc tgg gtc gaa cgc tgg				
286	Val Ser Glu Ala Thr Arg Ile Asp Pro Asn Ala Trp Val Glu Arg Trp				
287	765	770	775	780	
289	aag gcg gcg ggc cat tac cag gcc gaa gca gcg ttg ttg cag tgc acg				3844
290	Lys Ala Ala Gly His Tyr Gln Ala Glu Ala Ala Leu Leu Gln Cys Thr				
291	785	790	795		
292	gca gat aca ctt gct gat gcg gtg ctg att acg acc gct cac gcg tgg				3892
293	Ala Asp Thr Leu Ala Asp Ala Val Leu Ile Thr Ala His Ala Trp				
294	800	805	810		3940
296	cag cat cag ggg aaa acc tta ttt atc agc cg <sup>g</sup> aaa acc tac cgg att				
297	Gln His Gln Gly Lys Thr Leu Phe Ile Ser Arg Lys Thr Tyr Arg Ile				
298	815	820	825		3988
300	gat ggt agt ggt caa atg gcg att acc gtt gat gtt gaa gtg gcg agc				
301	Asp Gly Ser Gly Gln Met Ala Ile Thr Val Asp Val Glu Val Ala Ser				
302	830	835	840		4036
306	gat aca ccg cat ccg gcg att ggc ctg aac tgc cag ctg gcg cag				
307	Asp Thr Pro His Pro Ala Arg Ile Gly Leu Asn Cys Gln Leu Ala Gln				
308	845	850	855	860	
310	gta gca gag ccg gta aac tgg ctc gga tta ggg ccg caa gaa aac tat				4084
311	Val Ala Glu Arg Val Asn Trp Leu Gly Leu Gly Pro Gln Glu Asn Tyr				
312	865	870	875		
314	ccc gac cgc ctt act gcc gcc tgt ttt gac cgc tgg gat ctg cca ttg				4132
315	Pro Asp Arg Leu Thr Ala Ala Cys Phe Asp Arg Trp Asp Leu Pro Leu				
316	880	885	890		4180
318	tca gac atg tat acc ccg tac gtc ttc ccg agc gaa aac ggt ctg cgc				
319	Ser Asp Met Tyr Thr Pro Tyr Val Phe Pro Ser Glu Asn Gly Leu Arg				
320	895	900	905		
322	tgc ggg acg cgc gaa ttg aat tat-ggc cca cac cag tgg cgc ggc gac				
323	Cys Gly Thr Arg Glu Leu Asn Tyr Gly Pro His Gln Trp Arg Gly Asp				
324	910	915	920		
326	tcc cag ttc aac atc agc cgc tac agt caa cag caa ctg atg gaa acc				4228
327	Phe Gln Phe Asn Ile Ser Arg Tyr Ser Gln Gln Gln Leu Met Glu Thr				
328	925	930	935	940	
330	agc cat cgc cat ctg ctg cac gcg gaa gaa ggc aca tgg ctg aat atc				4324
331	Ser His Arg His Leu Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile				
332	945	950	955		
334	gac ggt ttc cat atg ggg att ggt ggc gac gac tcc tgg agc ccg tca				4372
335	Asp Gly Phe His Met Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro Ser				
336	960	965	970		
338	gta tcg gcg gaa ttc cag ctg agc gcc ggt cgc tac cat tac cag ttg				4420
339	Val Ser Ala Glu Phe Gln Leu Ser Ala Gly Arg Tyr His Tyr Gln Leu				
340	975	980	985		
342	gtc tgg tgt caa aaa aga tct gac tat aaa gat gag gac ctc gac cat				4468
343	Val Trp Cys Gln Lys Arg Ser Asp Tyr Lys Asp Glu Asp Leu Asp His				
344	990	995	1000		

**VERIFICATION SUMMARY**

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L:2112 M:283 W: Missing Blank Line separator, <220> field identifier